WHAT IS CLAIMED IS:

1. A nucleic acid molecule:
(i) having a nucleotide sequence capable of specifically hybridizing to the invariant proximal or invariant distal nucleotide sequence of a single nucleotide polymorphism, and
(ii) being used to specifically detect the single nucleotide polymorphic site (X) of the single nucleotide polymorphism.

2. The nucleic acid molecule of claim 1, wherein said mammal is selected from the group consisting of humans, non-human primates, dogs, cats, cattle, sheep, poultry, and horses.

3. The nucleic acid molecule of claim 2, wherein said mammal is a horse.

4. The nucleic acid molecule of claim 3, wherein said molecule has a nucleotide sequence selected from the group consisting of SEQ ID NO:(2n+1), wherein n is an integer selected from the group consisting of 0 through 35.

5. The nucleic acid molecule of claim 3, wherein the sequence of said immediately 3'-distal segment includes a sequence selected from the group consisting of SEQ ID NO:(2n+2), wherein n is an integer selected from the group consisting of 0 through 35.

6. A nucleic acid molecule having a sequence complementary to a sequence selected from the group consisting of SEQ ID NO:1 through SEQ ID NO:72 in Table 1.

7. A set of at least two of the nucleic acid molecules of claim 6.

8. A set of at least two nucleic acid molecules, wherein at least one of said nucleic acid molecules has a sequence complementary to a sequence selected from the group consisting of SEQ ID NO:1 through SEQ ID NO:72.

9. A method for determining the extent of genetic similarity between DNA of a target horse and DNA of a reference horse, which comprises the steps:

A) determining, for a single nucleotide polymorphism of said target horse, and for a corresponding single nucleotide polymorphism of said reference horse, whether said polymorphisms contain the same single nucleotide at their respective polymorphic sites; and

B) using said comparison to determine the extent of genetic similarity between said target horse and said reference horse.

10. The method of claim 9, wherein said polymorphic sites have (1) an immediately 5'-proximal sequence selected from the group consisting of SEQ ID NO:(2n+1), and (2) an immediately 3'-distal sequence selected from the group consisting of SEQ ID NO:(2n+2); wherein n is an integer selected from the group consisting of 0 through 35.

11. The method of claim 9, wherein in step A, said determination is sufficient to establish that said target horse and said reference horse are not the same animal.

12. The method of claim 9, wherein in step A, said determination is sufficient to establish that said reference horse is not a parent of said target horse.

13. The method of claim 9, wherein in step A, said reference horse has a trait, and said determination is sufficient to establish that said target horse also has said trait.

14. The method of claim 9, wherein in step A, said reference horse has a first and second trait, and said determination is sufficient to establish a genetic linkage between said traits.

15. The method of claim 9, wherein in step A, said determination is accomplished by a method having the sub-steps:
(a) incubating a sample of nucleic acid containing said single nucleotide polymorphism of said target horse, or said single nucleotide polymorphism of said reference horse, in the presence of a nucleic acid primer and at least one dideoxynucleotide derivative, under conditions sufficient to permit a polymerase mediated, template-dependent extension of said primer, said extension causing the incorporation of a single dideoxynucleotide to the 3'-terminus of said primer, said single dideoxynucleotide being complementary to the single nucleotide of the polymorphic site of said polymorphism;
(b) permitting said template-dependent extension of said primer molecule, and said incorporation of said single dideoxynucleotide; and
(c) determining the identity of the nucleotide incorporated into said polymorphic site, said identified nucleotide being complimentary to said nucleotide of said polymorphic site.

16. The method of claim 15, wherein in substep (a), said primer is immobilized to a solid support, and wherein in sub-step (b), said template-dependent extension of said primer is conducted on said immobilized primer.

17. The method of claim 15, wherein, in sub-step (a), said sample is processed to amplify a nucleic acid containing said polymorphism prior to said incubation.

18. The method of claim 15, wherein substep (a) additionally includes using a non-invasive swab to collect said sample of DNA from said horse.

19. The method of claim 15, wherein in substep (a), said polymerase mediated, template-dependent extension of said primer is conducted in the presence of at least two dideoxynucleotide triphosphate derivatives selected from the group consisting of ddATP, ddTTP, ddCTP and ddGTP, but in the absence of dATP, dTTP, dCTP and dGTP.

20. A method for determining the probability that a target horse will have a particular trait, which comprises the steps:

A) determining the identity of a single nucleotide present at a polymorphic site of an equine single nucleotide polymorphism, and being present in more than 51% of a set of reference horses;

B) determining whether a single nucleotide present at a polymorphic site of a corresponding single nucleotide polymorphism of said target horse has the same identity as the single nucleotide present at said polymorphic site of said 51% of reference horses exhibiting said trait;

C) using said determination of step B to establish the probability that said target horse will have said particular trait.

21. The method of claim 20, wherein said equine single nucleotide polymorphism has (1) an immediately 5'-proximal sequence selected from the group consisting of SEQ ID NO:(2n+1); and (2) an immediately 3'-distal sequence selected from the group consisting of SEQ ID NO:(2n+2); wherein n is an integer selected from the group consisting of 0 through 35.

22. The method of claim 20, wherein said trait is an equine genetic disease.

23. The method of claim 20, wherein said trait is an equine condition.

24. The method of claim 20, wherein said trait is an equine characteristic.

25. A method for creating a genetic map of unique sequence equine polymorphisms which comprises the steps:

A) identifying at least one pair of inter-breeding reference horses, wherein each of said pairs of horses is characterized by having a first and a second reference horse,

said first reference horse having:

two alleles (i) and (ii), said alleles each being single nucleotide polymorphic alleles having a single nucleotide polymorphic site;

said second reference horse having:

a corresponding allele (i') to said allele (i) of said first reference horse, wherein said allele (i') has a single nucleotide polymorphic site, and wherein the single nucleotide present at said polymorphic site of said allele (i') differs from the single nucleotide present at the polymorphic site of said allele (i) of said first reference horse, and

B) identifying in a progeny of at least one of said pairs of inter-breeding reference horses the single nucleotide present at a single nucleotide polymorphic site of a corresponding allele of said alleles (i) and (i'), and the single nucleotide present at a single nucleotide polymorphic site of a corresponding allele of said alleles (ii) and (ii'); and

C) determining the extent of genetic linkage between said alleles (i) and (ii), to thereby create said a genetic map.

26. The method of claim 25, wherein said steps A, B and C are repeated at least once in cycle, to thereby create a genetic map having more than two polymorphic sites.

27. The method of claim 25, wherein at least one of said alleles (i) and (ii) has (1) an immediately 5'-proximal sequence selected from the group consisting of SEQ ID NO:(2n+1); and (2) an immediately 3'-distal sequence selected from the group consisting of SEQ ID NO:(2n+2); wherein n is an integer selected from the group consisting of 0 through 35.

28. A method for predicting whether a target horse will exhibit a predetermined trait which comprises the steps:

A) identifying one or more alleles associated with said trait, each allele being a single nucleotide polymorphic allele having a single nucleotide polymorphic site;

B) determining for each of said single nucleotide polymorphic alleles, a nucleotide present at said alleles polymorphic site in a reference horse exhibiting said trait, to thereby define a set of single nucleotides at a set of polymorphic sites that are present in a reference horse exhibiting said trait;

C) determining the identity of single nucleotides present at corresponding single nucleotide polymorphic alleles of said target horse; and

D) comparing the identity of the single nucleotides present at the polymorphic sites of the polymorphisms of said reference animal with the single nucleotides present at said corresponding single nucleotide polymorphic alleles of said target horse.

29. The method of claim 28, wherein at least one of said polymorphisms has (1) an immediately 5'-proximal sequence selected from the group consisting of SEQ ID NO:(2n+1); and (2) an immediately 3'-distal sequence selected from the group consisting of SEQ ID NO:(2n+2); wherein n is an integer selected from the group consisting of 0 through 35.

30. A method for identifying a single nucleotide polymorphic site which comprises:

A) isolating a fragment of genomic DNA of a reference organism;

B) sequencing said fragment of DNA to thereby determine the nucleotide sequence of a segment of said fragment, said segment being of a length sufficient to define the nucleotide sequence of a pair of oligonucleotide primers capable of mediating the specific amplification of said fragment;

C) using said oligonucleotide primers to mediate the specific amplification of DNA obtained from a plurality of other organisms of the same species as said reference organism; and

D) determining the nucleotide sequences of said amplified DNA molecules of step C, and comparing the sequence of said amplified molecules with the sequence of said fragment of said reference organism to thereby identify a single nucleotide polymorphic site.

31. A method for interrogating a polymorphic region of a human single nucleotide polymorphism of a target human, said method comprising:

A) selecting a known human single nucleotide polymorphism for interrogation;

B) identifying the sequence of at least one oligonucleotide that flanks said selected single nucleotide polymorphism; said identified sequence being of a length sufficient to permit the identification of primers capable of being used

to effect the specific amplification of said flanking oligonucleotide and said polymorphism;

C) using said primers to effect the amplification of said flanking oligonucleotide and said polymorphism of said single nucleotide polymorphism of said target human; and

D) interrogating the single nucleotide polymorphism of said amplified polymorphism by genetic bit analysis.